

CRF Errors Corrected by the STIC Systems Branch

Serial Number: 10/024,607

CRF Processing Date: 1/22/2002
 Edited by: [Signature]
 Verified by: [Signature] (STIC staff)

ENTERED

- ☐ Changed a file from non-ASCII to ASCII
- ☐ Changed the margins in cases where the sequence text was "wrapped" down to the next line.
- ☐ Edited a format error in the Current Application Data section, specifically: #2
- ☐ Edited the Current Application Data section with the actual current number. The number inputted by the applicant was ☐ the prior application data; or ☐ other _____
- ☐ Added the mandatory heading and subheadings for "Current Application Data".
- ☐ Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.
- ☐ Changed the spelling of a mandatory field (the headings or subheadings), specifically: _____
- ☐ Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were: _____
- ☐ Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited: _____
- ☐ Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.
- ☐ Inserted colons after headings/subheadings. Headings edited included: _____
- ☐ Deleted extra, invalid, headings used by an applicant, specifically: _____
- ☒ Deleted: ☒ non-ASCII "garbage" at the beginning/end of files; ☐ secretary initials/filename at end of file; ☐ page numbers throughout text; ☐ other invalid text, such as _____
- ☐ Inserted mandatory headings, specifically: _____
- ☐ Corrected an obvious error in the response, specifically: _____
- ☐ Edited identifiers where upper case is used but lower case is required, or vice versa.
- ☐ Corrected an error in the Number of Sequences field, specifically: _____
- ☐ A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.
- ☐ Deleted **ending** stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected: _____
- ☒ Other: Seqs 9, 32 - inserted hard returns



OIFE

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/024,607

DATE: 01/22/2002

TIME: 19:28:41

Input Set : A:\Pto.amc

Output Set: N:\CRF3\01222002\J024607.raw

PS

3 <110> APPLICANT: Lee, Richard T.
 5 <120> TITLE OF INVENTION: CARDIOVASCULAR DISEASE DIAGNOSTIC AND THERAPEUTIC TARGETS
 7 <130> FILE REFERENCE: B0801/7231/ERP/KA
 C--> 9 <140> CURRENT APPLICATION NUMBER: US/10/024,607
 C--> 9 <141> CURRENT FILING DATE: 2001-11-08
 9 <150> PRIOR APPLICATION NUMBER: US 60/247,457
 10 <151> PRIOR FILING DATE: 2000-11-09
 12 <160> NUMBER OF SEQ ID NOS: 33
 14 <170> SOFTWARE: FastSEQ for Windows Version 3.0
 16 <210> SEQ ID NO: 1
 17 <211> LENGTH: 2586
 18 <212> TYPE: DNA
 19 <213> ORGANISM: Rattus norvegicus
 21 <220> FEATURE:
 22 <221> NAME/KEY: mRNA
 23 <222> LOCATION: (1)...(2586)
 24 <223> OTHER INFORMATION: Fit-1S
 26 <400> SEQUENCE: 1
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 28 cttcccagcc cttcatctgg gctacactga tttctctttt ggaccctaca tcagacagca 120
 29 cacatcaacc gcctagtggg ctcaccgtta ctttctgtg ccattgccat cggagagatc 180
 30 tgggccatca atcactagca catgattggc aaatggagaa tggggctttg ggctttggca 240
 31 attctgacag ttcccatgta tttcatagt acagagggca gaaaaacatc ctgggggtcta 300
 32 gaaaacgagg ctttaattgt cagatgcccc caaagaggag gtgcgattaa ccctgtggaa 360
 33 tgggtattatt caaatacaaa tgaaagaatt cctactcaaa agagaaatcg gatcttcgtc 420
 34 tcaagagatc gtctgaagtt tctaccagcc aaagtggag actctgggat ttatacgtgt 480
 35 gttatcagaa gccctgaatc gattaagacc ggatctttga atgtcaccat atataaaaaga 540
 36 ccaccaaact gcaaaatccc tgattacatg atgtactcga cagtagatgg atcagataaa 600
 37 aattccaaga taacatgtcc aacaattgcc ttgtataatt ggacagcgcc tgttcagtgg 660
 38 ttttaagaact gcaaagctct ccaagggcca aggttcaggg cacacatgtc ctatttggtc 720
 39 attgacaaag tgagtcatgt tgatgaaggt gactacacat gtcgattcac tcacacggag 780
 40 aacggaacca attacattgt gactgccacc agatcattca cagttgaaga aaaaggcttc 840
 41 tctacatttc cagtaattac aaacctcca cacaactaca cagtggaggt ggaaatagga 900
 42 aaaacagcaa acattgcctg ctcagcttgc tttggcacag cctctcagtt cgttgctgtc 960
 43 ctgtggcaga ttaacaaaac gagaattgga tcttttggca aagcaagaat tcaagaagag 1020
 44 aaaggcccaa ataaaagtcc cagcaatggc atgatttgct taacctcact gttaaggata 1080
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 50 ctgtcttcta gaaggactct ctgtcattgt atctttcctc tctctgtttc cccttgcct 1440
 51 tgttctctc acggtcctcc ccatcccttc accttctctc acgttctctc tactcttctt 1500

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Output Set: N:\CRF3\01222002\J024607.raw

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54 ccctttgtga ctcttgtaac agaaaacaac ttacacatta ggtggatgac caacttgatc 1680
55 ccattttaaa agagtagaga aaacatgata tttttaccct taacactctc ttatgatact 1740
56 aaccactgcc tcaatggcaa tacaactaat gtaaaaacat tattttaact tctttcaaat 1800
57 atcaagaggg tgtggaaggg agagagacac tgactctaag ctcatagtga tatgtggggc 1860
58 atttattggg attaagatat tgattaaatg attaggggtg gggtagctat tggataccat 1920
59 caagctgtgt cactgcctga agtggtagt gggatttttt tttggttctg tttgtcttct 1980
60 ttggtttgtt ttaactatag agaccattct gctcttgaac tcctagagtt ccacctggct 2040
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62 gttttggttt caattttaga gcctctggct tgtaagattt ttataaagta gagtttgatt 2160
63 cataggtggc cagagttgtg actcatagat gggttttagt gaggtcttag gcatccaccc 2220
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65 ggtcatggca cattctatag gaaaagagaa gccaaagccc tagtctcacc aggcacaacc 2340
66 ttgagtcctc actgctctcc tctgccaaac ggaccttttg tccagatttc tgagtattct 2400
67 ctagttacat ttgtatttga actatatttg tgttatctgt aattctgtat ttgttttgtt 2460
68 tgtgtgtggt tttgtatttt ccagattatt tttaattcac ctgttgctat tcaaataaat 2520
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70 atgata 2586

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72 <210> SEQ ID NO: 2

73 <211> LENGTH: 336

74 <212> TYPE: PRT

75 <213> ORGANISM: Rattus norvegicus

77 <220> FEATURE:

78 <221> NAME/KEY: PEPTIDE

79 <222> LOCATION: (1)...(336)

80 <223> OTHER INFORMATION: Fit-1S

82 <400> SEQUENCE: 2

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86 20 25 30
87 Leu Glu Asn Glu Ala Leu Ile Val Arg Cys Pro Gln Arg Gly Gly Ala
88 35 40 45
89 Ile Asn Pro Val Glu Trp Tyr Tyr Ser Asn Thr Asn Glu Arg Ile Pro
90 50 55 60
91 Thr Gln Lys Arg Asn Arg Ile Phe Val Ser Arg Asp Arg Leu Lys Phe
92 65 70 75 80
93 Leu Pro Ala Lys Val Glu Asp Ser Gly Ile Tyr Thr Cys Val Ile Arg
94 85 90 95
95 Ser Pro Glu Ser Ile Lys Thr Gly Ser Leu Asn Val Thr Ile Tyr Lys
96 100 105 110
97 Arg Pro Pro Asn Cys Lys Ile Pro Asp Tyr Met Met Tyr Ser Thr Val
98 115 120 125
99 Asp Gly Ser Asp Lys Asn Ser Lys Ile Thr Cys Pro Thr Ile Ala Leu
100 130 135 140
101 Tyr Asn Trp Thr Ala Pro Val Gln Trp Phe Lys Asn Cys Lys Ala Leu
102 145 150 155 160
103 Gln Gly Pro Arg Phe Arg Ala His Met Ser Tyr Leu Phe Ile Asp Lys

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104                               165                               170                               175
105 Val Ser His Val Asp Glu Gly Asp Tyr Thr Cys Arg Phe Thr His Thr
106                               180                               185                               190
107 Glu Asn Gly Thr Asn Tyr Ile Val Thr Ala Thr Arg Ser Phe Thr Val
108                               195                               200                               205
109 Glu Glu Lys Gly Phe Ser Thr Phe Pro Val Ile Thr Asn Pro Pro His
110                               210                               215                               220
111 Asn Tyr Thr Val Glu Val Glu Ile Gly Lys Thr Ala Asn Ile Ala Cys
112                               225                               230                               235                               240
113 Ser Ala Cys Phe Gly Thr Ala Ser Gln Phe Val Ala Val Leu Trp Gln
114                               245                               250                               255
115 Ile Asn Lys Thr Arg Ile Gly Ser Phe Gly Lys Ala Arg Ile Gln Glu
116                               260                               265                               270
117 Glu Lys Gly Pro Asn Lys Ser Ser Ser Asn Gly Met Ile Cys Leu Thr
118                               275                               280                               285
119 Ser Leu Leu Arg Ile Thr Gly Val Thr Asp Lys Asp Phe Ser Leu Lys
120                               290                               295                               300
121 Tyr Asp Cys Val Ala Met Asn His His Gly Val Ile Arg His Pro Val
122                               305                               310                               315                               320
123 Arg Leu Arg Arg Lys Gln Pro Ser Lys Glu Cys Leu Ser Gln Ile Ala
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127 <211> LENGTH: 2065

128 <212> TYPE: DNA

129 <213> ORGANISM: Rattus norvegicus

131 <220> FEATURE:

132 <221> NAME/KEY: mRNA

133 <222> LOCATION: (1)...(2065)

134 <223> OTHER INFORMATION: Fit-1M

136 <400> SEQUENCE: 3

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139 agatgcacct acccggcagg ggtgaaatcc caagctacac tgatttctct tttggaccct      180
140 acatcagaca gcacacatca accgcctagt ggactcaccg ttaccttctt gtgccattgc      240
141 catcggagag atctcggcca tcaatcacta gcacatgatt ggcaaatgga gaatggggct      300
142 ttgggctttg gcaattctga cagttcccat gtatttcata gtgacagagg gcagaaaaac      360
143 atcctggggg ctagaaaacg aggctttaat tgtcagatgc ccccaaagag gaggtgcgat      420
144 taacctgtg gaattggtatt attcaaatac aaatgaaaga attcctactc aaaagagaaa      480
145 tcggatcttc gtctcaagag atcgtctgaa gtttctacca gccaaagtgg aagactctgg      540
146 gatttatacg tgtgttatca gaagccctga atcgattaag accggatctt tgaatgtcac      600
147 catatataaa agaccaccaa actgcaaaat ccctgattac atgatgtact cgacagtaga      660
148 tggatcagat aaaaattcca agataacatg tccaacaatt gccttgata attggacagc      720
149 gcctgttcag tggtttaaga actgcaaagc tctccaaggg ccaaggttca gggcacacat      780
150 gtctattttg ttcatgaca aagtgagtca tgttgatgaa ggtgactaca catgtcgatt      840
151 cactcacacg gagaacggaa ccaattacat tgtgactgcc accagatcat tcacagttga      900
152 agaaaaaggc ttctctacat ttccagtaat taaaaaccct ccacacaact acacagtgga      960
153 agtggaaata ggaaaaacag caaacattgc ctgctcagct tgctttggca cagcctctca     1020
154 gttcgttgct gtcctgtggc agattaacaa aacgagaatt ggatcttttg gcaaagcaag     1080
155 aattcaagaa gagaaaggcc caaataaaag ttccagcaat ggcatgattt gcttaacctc     1140

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156 actgttaagg ataactggtg tgaccgacaa ggacttctcc ctgaaatatg actgtgtggc 1200
157 catgaaccat cacggagtga taaggcacc cgtgaagactg agaaggaaac aaccaattga 1260
158 ccaccaaagc acctactaca tagttgccg atgtagttta ttgctaattg ttatcaatgt 1320
159 cttggtgata gtcttaaaag tgttctggat tgaggttgct ctgttctgga gagatataat 1380
160 ggcaccttac aaaaccaga atgatggaaa gctctatgat gcttacatca tttaccctcg 1440
161 ggtcttccgg ggcagcgcag cagggaccgg ctctgtggag tactttgttc actacactct 1500
162 gcccgacgtt ctgaaaata aatgtggcta caagttgtgc atttacggga gagacctgct 1560
163 gcctgggcaa gatgcggcca ctgtggtgga aagcagtatc cagaatagta gacggcaagt 1620
164 gtttgtcctg gccctcaca tgatgcacag caaagagttt gcctatgagc aggagatcgc 1680
165 cctgcacagc gccctcatcc agaacaactc caaggtgatt ctgattgaaa tggagcctat 1740
166 ggggtgaggca agccgactgc agcttgggga tctgcaagat tctctccagc atcttgtgaa 1800
167 aatgcagggg accatcaagt ggaggggaaga ccacgtggcc gacaaacagt ctctaagctc 1860
168 caaattctgg aagcatgtga gataccaaat gccagtcctg aaaagacccc ccaagatggc 1920
169 atctgttgcc gctccgttga gtggcaagggt gtgcttggac ctgaaacact tttgagtcgt 1980
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173 <210> SEQ ID NO: 4
174 <211> LENGTH: 566
175 <212> TYPE: PRT
176 <213> ORGANISM: Rattus norvegicus
178 <220> FEATURE:
179 <221> NAME/KEY: PEPTIDE
180 <222> LOCATION: (1)...(566)
181 <223> OTHER INFORMATION: Fit-1M
183 <400> SEQUENCE: 4
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188 Leu Glu Asn Glu Ala Leu Ile Val Arg Cys Pro Gln Arg Gly Gly Ala
189 35 40 45
190 Ile Asn Pro Val Glu Trp Tyr Tyr Ser Asn Thr Asn Glu Arg Ile Pro
191 50 55 60
192 Thr Gln Lys Arg Asn Arg Ile Phe Val Ser Arg Asp Arg Leu Lys Phe
193 65 70 75 80
194 Leu Pro Ala Lys Val Glu Asp Ser Gly Ile Tyr Thr Cys Val Ile Arg
195 85 90 95
196 Ser Pro Glu Ser Ile Lys Thr Gly Ser Leu Asn Val Thr Ile Tyr Lys
197 100 105 110
198 Arg Pro Pro Asn Cys Lys Ile Pro Asp Tyr Met Met Tyr Ser Thr Val
199 115 120 125
200 Asp Gly Ser Asp Lys Asn Ser Lys Ile Thr Cys Pro Thr Ile Ala Leu
201 130 135 140
202 Tyr Asn Trp Thr Ala Pro Val Gln Trp Phe Lys Asn Cys Lys Ala Leu
203 145 150 155 160
204 Gln Gly Pro Arg Phe Arg Ala His Met Ser Tyr Leu Phe Ile Asp Lys
205 165 170 175
206 Val Ser His Val Asp Glu Gly Asp Tyr Thr Cys Arg Phe Thr His Thr
207 180 185 190

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Input Set : A:\Pto.amc

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208  Glu Asn Gly Thr Asn Tyr Ile Val Thr Ala Thr Arg Ser Phe Thr Val
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210  Glu Glu Lys Gly Phe Ser Thr Phe Pro Val Ile Thr Asn Pro Pro His
211              210              215              220
212  Asn Tyr Thr Val Glu Val Glu Ile Gly Lys Thr Ala Asn Ile Ala Cys
213  225              230              235              240
214  Ser Ala Cys Phe Gly Thr Ala Ser Gln Phe Val Ala Val Leu Trp Gln
215              245              250              255
216  Ile Asn Lys Thr Arg Ile Gly Ser Phe Gly Lys Ala Arg Ile Gln Glu
217              260              265              270
218  Glu Lys Gly Pro Asn Lys Ser Ser Ser Asn Gly Met Ile Cys Leu Thr
219              275              280              285
220  Ser Leu Leu Arg Ile Thr Gly Val Thr Asp Lys Asp Phe Ser Leu Lys
221              290              295              300
222  Tyr Asp Cys Val Ala Met Asn His His Gly Val Ile Arg His Pro Val
223  305              310              315              320
224  Arg Leu Arg Arg Lys Gln Pro Ile Asp His Gln Ser Thr Tyr Tyr Ile
225              325              330              335
226  Val Ala Gly Cys Ser Leu Leu Leu Met Phe Ile Asn Val Leu Val Ile
227              340              345              350
228  Val Leu Lys Val Phe Trp Ile Glu Val Ala Leu Phe Trp Arg Asp Ile
229              355              360              365
230  Met Ala Pro Tyr Lys Thr Gln Asn Asp Gly Lys Leu Tyr Asp Ala Tyr
231              370              375              380
232  Ile Ile Tyr Pro Arg Val Phe Arg Gly Ser Ala Ala Gly Thr Gly Ser
233  385              390              395              400
234  Val Glu Tyr Phe Val His Tyr Thr Leu Pro Asp Val Leu Glu Asn Lys
235              405              410              415
236  Cys Gly Tyr Lys Leu Cys Ile Tyr Gly Arg Asp Leu Leu Pro Gly Gln
237              420              425              430
238  Asp Ala Ala Thr Val Val Glu Ser Ser Ile Gln Asn Ser Arg Arg Gln
239              435              440              445
240  Val Phe Val Leu Ala Pro His Met Met His Ser Lys Glu Phe Ala Tyr
241              450              455              460
242  Glu Gln Glu Ile Ala Leu His Ser Ala Leu Ile Gln Asn Asn Ser Lys
243  465              470              475              480
244  Val Ile Leu Ile Glu Met Glu Pro Met Gly Glu Ala Ser Arg Leu Gln
245              485              490              495
246  Leu Gly Asp Leu Gln Asp Ser Leu Gln His Leu Val Lys Met Gln Gly
247              500              505              510
248  Thr Ile Lys Trp Arg Glu Asp His Val Ala Asp Lys Gln Ser Leu Ser
249              515              520              525
250  Ser Lys Phe Trp Lys His Val Arg Tyr Gln Met Pro Val Pro Lys Arg
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252  Pro Pro Lys Met Ala Ser Val Ala Ala Pro Leu Ser Gly Lys Val Cys
253  545              550              555              560
254  Leu Asp Leu Lys His Phe
255              565
257 <210> SEQ ID NO: 5

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VERIFICATION SUMMARY

PATENT APPLICATION: US/10/024,607

DATE: 01/22/2002

TIME: 19:28:42

Input Set : A:\Pto.amc

Output Set: N:\CRF3\01222002\J024607.raw

L:9 M:270 C: Current Application Number differs, Replaced Current Application No

L:9 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:1402 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:26